

PP-196 A case of imported hepatitis E in Japan

Manri Kawakami^{*,1,2}, Kumiyo Ashida^{3,4}, Natsumi Abe^{5,6}, Kazuaki Takahashi^{5,6}, Shunji Mishiro^{5,6}. ¹Clinical Research Center; ²Kurashiki Medical Hospital; ³Department of Internal Medicine; ⁴Kato City Hospital; ⁵Department of medical Sciences; ⁶Toshiba General Hospital

Background: In Japan, hepatitis E is considered as “imported infection” by travelers back from endemic areas or zoonotic transmission by eating law meat of pigs, boars, deer et al. Recently, we can identify the location of HEV infection by molecular epidemiological approach. We will describe a Japanese case of imported hepatitis E and usefulness of molecular approach.

Case: A 56-year-old man was admitted to Kato City Hospital with jaundice, fever and general malaise on November 26, 2007. He had worked in China (Mushaku City) for four years and four days before he came back to Japan and felt abnormal condition. Laboratory tests showed abnormal liver function tests (AST 5456 IU/L, ALT 5236 IU/L, TB1.72mg/dl, PT 55%). The skin appeared jaundiced and eruptions. Conservative management improved his conditions and laboratory data and he was discharged one month later. He had IgM class antibodies to HEV and detectable HEV RNA of genotype IV. Its nucleotide sequences of HEV showed quite a high degree of similarity to the reported in China.

Analysis and Conclusion: In Japan, 23 imported hepatitis E cases were previously reported and 15 cases were checked HEV genotype by PCR. There were mainly two patterns. One was infected in India-Nepal-Pakistan area and all belongs to genotype I. The other was infected in China and genotype IV. As the Japanese travelers to abroad increased, the number of the imported cases with hepatitis E will be increased. But identification of the infected location was possible.

PP-197 Identification of an isolate from a patient with suspected scrub typhus

Lijuan Zhang^{*,1}, Feng Cui², Lingling Zhang², Lingling Wang². ¹National Institute of Communicable Disease Control and Prevention, China CDC; ²Zibo Center for Disease Control & Prevention, Zibo, Shandong, China

Rickettsioses are worldwide zoonoses that continue to cause severe illness and death in healthy adults and children. Here we report one case with spotted fever confirmed by Shell vial culture.

A 61-year-old woman presented to the Yiyuan county hospital with eight-day fever (38–39° on Oct 31, 2007). Scrub typhus was diagnosed based on the clinical characterization. 0.5ml sodium citrate anticoagulant blood was inoculated into L929 cells contained in sell vial culture bottles. PCR amplification of 16SrRNA, *gltA*, 17KD, *ompA* and *groEL* genes of the isolate showed expected bands. Sequence analysis of 16SrRNA gene products (879bp) demonstrated 100% of similarity to *R. heilongjiangii* 054, *R. japonica* and another Chinese isolate (GDM18). The *gltA* gene (335bp) showed 100% similarity to *R. japonica* but 99% similarity to *R. raoultii* and *R. heilongjiangii* 054. *OmpA* gene sequence (575bp) was 100% similarity to *R. heilongjiangii* 054 and 17KD gene (317bp) showed 97% similarity to another two Chinese isolates (GDM15 and GDM17) respectively. *GroEL* gene (582bp) showed 100% similarity to *R. heilongjiangii* 054, Hainan 1, GDM 3 respectively. We isolated a spotted fever group rickettsia from a clinical diagnosed scrub typhus. We emphasize on differential diagnose of rickettsioses in clinical practice and future surveillance of rickettsiosis should focus on culturing the microorganism.

PP-198 Differentially expressed genes between female and male adult *Anopheles anthropophagus*

Yijie Geng, Shitong Gao, Dana Huang, Xiaoheng Li, Yirui Zhao, Renli Zhang*. Shenzhen Center for Disease Control and Prevention

Object: The aim of the present study was to identify sex-specific genes in adult *Anopheles anthropophagus*.

Methods: A subtractive cDNA library for female *Anopheles anthropophagus* was constructed using the Suppression Subtractive Hybridization (SSH) technique and then 3074 clones from the female SSH library were analyzed using a microarray-based survey. Genes that were expressed differentially according to gender in *Anopheles anthropophagus* were screened using Real-Time PCR and RT-PCR.

Results: We reported a series of genes which may be involved in female-specific mosquito behavior, including an inorganic phosphate transporter, a serine protease, the salivary protein GP35-2 and the D7 cluster salivary protein.

Conclusion: The complex behavior which only female *Anopheles* mosquitoes take blood meals and transmit pathogens may be initiated by the genetic background behind the sexual difference.

Poster Presentation – Tuberculosis**PP-199 Effect of treatment and bacterial status on T cell response to *Mycobacterium tuberculosis* specific antigens in Chinese active tuberculosis patients**

Shu Zhang^{*,1}, Wenhong Zhang¹, Lingyun Shao¹, Ling Mo¹, Jiazhen Chen¹, Feifei Wang¹, Chengyan Meng¹, Ming Zhong², Lihua Qiu³, Meiyong Wu⁴, Xinhua Weng¹. ¹Department of Infectious Diseases, Huashan Hospital, Fudan University, Shanghai, China; ²Department of Tuberculosis, Chongqing Pulmonary Hospital, Chongqing, China; ³Department of Tuberculosis, Shandong Chest Hospital, Jinan, Shandong province, China; ⁴Department of Tuberculosis Infection, Suzhou No. 5 People's Hospital, Suzhou, Jiangsu province, China

Objectives: To evaluate the diagnostic power compared with TST and dynamic *M.tb*-specific T-cell responses of active TB cases with treatment durations, we conducted a cross-sectional study in high-epidemic regions of China.

Methods: Eighty-nine patients with active pulmonary TB (ATB) and 57 healthy controls (HC) were recruited and tested with TST, T-SPOT.TB, acid-fast smear of sputum and *M.tb* culture.

Results: Eighty-nine patients with active pulmonary TB receiving initial anti-TB treatment were divided into 3 subgroups: 0-1 mo, 1-3 mo and 3-6 mo, in which the positive rates of T-SPOT.TB assay were 94.4%, 86.4% and 61.5%, respectively. The positive rate of T-SPOT.TB assay declined with the duration of anti-TB treatment, which was significantly lower in 3-6 mo group than in 0-1 mo group ($P<0.005$). Forty-one ATB patients with anti-TB treatment equal or shorter than 1 month were divided into two subgroups based on the results of acid-fast smear of sputum and *M.tb* culture: Bacteriology (+) and Bacteriology (–). The positive rate of T-SPOT.TB assay in Bacteriology (+) group was similar to that in Bacteriology (–) group (93.10% vs. 100.00%, $P=1.000$), whereas HC group had the lowest positive rate of T-SPOT.TB assay (21.05%, $P=0.000$).

Conclusion: Interferon- γ -release assays (IGRAs) may act as a predictive marker for anti-TB treatment in both active and latent TB infection and the bacterial status of ATB patient doesn't affect IGRA results.